SEQUENCE LISTING

#9

<110> Hasse, Detlef
Panaccio, Michael
Sinistaj, Meri

<120> LAWSONIA DERIVED GENE AND RELATED OMPH POLYPEPTIDES, PEPTIDES, AND PROTEINS AND THEIR USES

<130> DAVI149.001APC

<140> US 10/018,290
<141> 2001-11-13

<150> PCT/AU00/00438
<151> 2000-05-11

<150> US 60/133,986
<151> 1999-05-13

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 186
<212> PRT
<213> Lawsonia intracellularis

<400> 1

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Met Lys Val Lys Thr Leu Ser Met Ala Ile Leu Ala Cys Leu Leu Val
 1               5                  10                  15
Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
            20                  25                  30
Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
        35                  40                  45
Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
    50                  55                  60
Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
65                  70                  75                  80
Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
                85                  90                  95
Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
            100                 105                 110
Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
        115                 120                 125
Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
    130                 135                 140
Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
145                 150                 155                 160
Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
                165                 170                 175
Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
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180 185

<210> 2
<211> 561
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (1)...(561)

<400> 2

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atg aaa gta aaa act ctt tcc atg gct att tta gct tgt tta tta gta   48
Met Lys Val Lys Thr Leu Ser Met Ala Ile Leu Ala Cys Leu Leu Val
 1               5                  10                  15

gct aac agt gca ttt tcg gct gac ttc cct att ggt gtc ttt aat tct   96
Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
            20                  25                  30

caa tcc att gcc atg gag agt gaa gca gct aag gcc gct caa aaa aaa   144
Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
        35                  40                  45

tta caa tca gaa ttt ggt aat gaa aaa aca caa ctt gaa aaa caa gca   192
Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
    50                  55                  60

aaa gat ttg caa aca aaa gct gat gat tta caa gct aag tca gca gct   240
Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
65                  70                  75                  80

atg tct aac caa gca cgt gaa gat aaa caa aga gaa ttt ctt gaa ctt   288
Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
                85                  90                  95

cgt cgt aat ttc gaa gaa aaa tct cgt gac ttt gca ata cgt gtc gaa   336
Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
            100                 105                 110

caa gct gaa aac aca tta cgt caa tat cta gct gaa caa atc tat ctt   384
Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
        115                 120                 125

gct gct gaa act ata gca aaa aag aaa ggg tta aaa ctt gtt ctt gat   432
Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
    130                 135                 140

agt gct agt gga agt gta atg tac ctt gaa aaa aat cta gat att aca   480
Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
145                 150                 155                 160

aaa gaa att ctt gaa gcc ata aat gct gca tgg aaa aaa ggt gga agt   528
Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
```

```
                165                 170                 175

aaa ctt cca gag atg gca aac cgg aaa aaa taa                          561
Lys Leu Pro Glu Met Ala Asn Arg Lys Lys  *
            180                 185
```

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer RA176 forward

<400> 3
tttattcatt cagaaggagc ttc 23

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer RA177 reverse

<400> 4
aagtttagca atttctgaaa g 21

<210> 5
<211> 143
<212> PRT
<213> Yersinia pseudotuberculosis

<400> 5

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Ser Ser Ile Phe Gln Gln Leu Pro Ala Arg Glu Ala Val Ala Ala Gly
 1               5                  10                  15
Lys Lys Gln Leu Glu Asn Glu Phe Lys Gly Arg Ala Thr Glu Leu Gln
            20                  25                  30
Gly Ile Ala Ile Val Asn Val Met Glu Arg Asp Leu Gln Thr Lys Met
        35                  40                  45
Gln Lys Leu Gln Arg Asp Gly Ser Thr Met Lys Ala Ser Asp Arg Thr
    50                  55                  60
Lys Ile Leu Ser Arg Ile Gln Asp Ala Val Lys Ser Val Ala Thr Leu
65                  70                  75                  80
Glu Asn Glu Val Met Lys Gln Arg Glu Thr Lys Gly Gly Tyr Asp Val
                85                  90                  95
Val Ile Asp Ala Asn Ala Val Ala Tyr Ala Asp Ser Ser Phe Ser Thr
            100                 105                 110
Lys Ala Gln Ala Phe Glu Gln Asp Asn Arg Arg Arg Gln Ala Glu Glu
        115                 120                 125
Arg Asn Lys Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val Lys
    130                 135                 140
```

<210> 6
<211> 164
<212> PRT
<213> Yersinia enterocolitica

<400> 6
Met Lys Lys Ser Ser Ile Phe Gln Gln Leu Pro Ala Arg Glu Thr Val
 1   5   10   15
Ala Trp Leu Cys Ala Ala Ser Leu Gly Leu Ala Leu Ala Ala Ser Ala
            20   25   30
Arg Val Gln Ala Ala Lys Ile Lys Gln Leu Glu Asn Glu Phe Lys Gly
        35   40   45
Arg Ala Thr Glu Leu Gln Gly Ala Ile Val Asn Val Met Glu Arg Asp
    50   55   60
Leu Gln Thr Lys Met Gln Lys Leu Gln Arg Asp Gly Ser Thr Met Lys
65   70   75   80
Ala Ser Asp Arg Thr Lys Ile Leu Ser Arg Ile Gln Asp Ala Val Lys
                85   90   95
Ser Val Ala Ser Leu Glu Asn Asp Val Met Lys Gln Arg Glu Thr Lys
            100   105   110
Gly Gly Tyr Asp Val Val Ile Asp Ala Asn Ala Val Ala Tyr Ala Asp
        115   120   125
Pro Ser Phe Ser Thr Lys Ala Gln Ala Phe Glu Gln Asp Asn Arg Arg
    130   135   140
Arg Gln Met Glu Glu Arg Asn Lys Lys Asp Ile Thr Ala Asp Val Leu
145   150   155   160
Lys Gln Val Lys

<210> 7
<211> 197
<212> PRT
<213> Haemophilus influenzae

<400> 7
Met Lys Asn Ile Gly Tyr Ile Phe Gln His His Pro Asp Arg Gln Ala
 1   5   10   15
Val Ala Ala Lys Val Thr Ala Leu Ala Leu Gly Ile Ala Leu Ala Ser
            20   25   30
Gly Tyr Ala Ser Ala Glu Glu Lys Asp Lys Leu Asp Ala Glu Phe Lys
        35   40   45
Pro Val Ala Glu Lys Leu Ala Ala Ser Lys Ile Ala Phe Ile Asn Ala
    50   55   60
Lys Glu Val Asp Asp Lys Ile Ala Ala Ala Arg Lys Lys Val Glu Ala
65   70   75   80
Lys Val Ala Ala Leu Glu Lys Asp Ala Pro Arg Leu Arg Gln Ala Asp
                85   90   95
Ile Gln Lys Leu Leu Asp Ser Ile Gln Thr Ala Thr Asn Asn Leu Ala
            100   105   110
Lys Arg Gln Gln Glu Ile Asn Lys Leu Gly Ala Ala Glu Asp Ala Glu
        115   120   125
Leu Gln Lys Leu Met Gln Glu Ala Lys Gly Tyr Thr Tyr Val Leu Asp
    130   135   140
Ala Asn Ser Ile Val Phe Ala Val Glu Gly Leu Arg Lys Leu Gln Val

145 150 155 160
Glu Ala Gln Ser Lys Leu Ser Arg Lys Lys Ala Glu Leu Glu Lys Met
165 170 175
Lys Asp Ile Thr Glu Glu Val Leu Lys Ser Ile Pro Ala Ser Glu Lys
180 185 190
Ala Gln Glu Lys Lys
195

<210> 8
<211> 162
<212> PRT
<213> Aquifex aeolicus

<400> 8
Met Glu Gly Asn Lys Val Ile Arg Glu Ser Lys Phe Ile Ala Lys Ala
1 5 10 15
Gln Ile Met Lys Lys Phe Phe Ala Leu Met Thr Leu Ile Ala Gly Ile
20 25 30
Ser Phe Ser Leu Asp Thr Glu Leu Arg Lys Glu Leu Glu Lys Tyr Gln
35 40 45
Lys Leu Ile Gln Glu Phe Ala Cys Val Asp Thr Lys Gln Lys Lys Leu
50 55 60
Glu Ala Leu Lys Lys Ser Leu Glu Ser Lys Ala Leu Ser Glu Lys Ala
65 70 75 80
Lys Glu Lys Val Phe Asp Lys Val Ile Lys Ile Val Glu Ser Thr Ala
85 90 95
Lys Lys Ala Lys Glu Ile Glu Gln Leu Glu Asp Glu Lys Lys Lys Ile
100 105 110
Lys Ala Val Phe Asp Cys Asn Ser Met Leu Tyr Trp Asp Lys Lys Leu
115 120 125
Arg Lys Leu Gln Val Glu Ala Gln Ser Lys Leu Ser Arg Lys Lys Ala
130 135 140
Glu Leu Glu Lys Met Ile Asp Ile Thr Asn Glu Val Leu Lys Glu Leu
145 150 155 160
Asp Lys

<210> 9
<211> 161
<212> PRT
<213> Escherichia coli

<400> 9
Met Lys Lys Gly Ser Leu Phe Gln Gln Val Ala Gln Lys Thr Gly Val
1 5 10 15
Ser Trp Leu Leu Ala Ala Gly Leu Gly Leu Ala Leu Ala Thr Ser Ala
20 25 30
Gln Ala Ala Asp Lys Ile Asn Thr Leu Glu Asn Glu Phe Lys Gly Arg
35 40 45
Ala Ser Glu Leu Gln Arg Ala Ile Val Asn Met Met Glu Thr Asp Leu
50 55 60
Gln Ala Lys Met Lys Lys Leu Gln Ser Met Lys Ala Gly Ser Asp Arg
65 70 75 80

```
Thr Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala Asn
                85                  90                  95
Leu Glu Lys Asp Val Met Ala Gln Arg Gln Thr Ser Gln Asp Ile Asp
            100                 105                 110
Leu Val Val Asp Ala Asn Ala Val Ala Tyr Asn Ser Ser Asp Val Phe
        115                 120                 125
Ala Gln Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn
    130                 135                 140
Glu Glu Arg Gly Lys Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
145                 150                 155                 160
Lys
```

<210> 10
<211> 161
<212> PRT
<213> Streptococcus typhi

<400> 10

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Met Lys Lys Gly Asn Leu Phe Gln Gln Val Ala Gln Lys Thr Gly Val
 1               5                  10                  15
Ser Trp Leu Leu Ala Ala Gly Leu Gly Leu Ala Met Val Thr Ser Ala
            20                  25                  30
Gln Ala Ala Asp Lys Ile Asn Thr Leu Glu Asn Glu Phe Lys Gly Arg
        35                  40                  45
Ala Ala Glu Leu Gln Lys Ala Ile Val Asn Met Met Glu Thr Asp Leu
    50                  55                  60
Gln Ser Lys Met Gln Arg Leu Gln Ser Met Lys Ala Gly Ser Asp Arg
65                  70                  75                  80
Thr Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Lys Val Ala Asn
                85                  90                  95
Leu Glu Lys Asp Val Met Ser Gln Arg Gln Thr Asp Gln Ser Ile Asp
            100                 105                 110
Leu Val Val Asp Ala Asn Thr Val Ala Tyr Asn Ser Ser Asp Val Phe
        115                 120                 125
Ala Gln Lys Ala Gln Ala Phe Glu Lys Asp Arg Ala Arg Arg Ser Asn
    130                 135                 140
Glu Glu Arg Asn Lys Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
145                 150                 155                 160
Lys
```

<210> 11
<211> 177
<212> PRT
<213> Chlamidia trachomatis

<400> 11

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Met Lys Lys Phe Arg Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys
 1               5                  10                  15
Glu Ser Leu Leu Leu Ser Leu Met Ser Leu Ser Ser Leu Pro Thr Phe
            20                  25                  30
Ala Ala Asn Ser Thr Gly Thr Ala Glu Phe Glu Lys Met Lys Asn Gln
```

```
        35                  40                  45
Phe Ser Asn Ser Met Gly Lys Ile Gly Ile Val Asn Leu Met Glu Glu
    50                  55                  60
Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu
65                  70                  75                  80
Gly Leu Ser Glu Thr Ala Ala Ala Glu Ile Met Glu Glu Val Lys Lys
                85                  90                  95
Ala Ser Glu Thr Val Arg Ile Leu Arg Lys Lys Phe Glu Asp Leu Ser
            100                 105                 110
Ala Glu Gln Glu Gly Leu Ser Val Leu Leu Asn Glu Asp Ile Val Leu
        115                 120                 125
Ser Ile Asp Ser Ser Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile
    130                 135                 140
Leu Asn Gln Ser Asn Leu Lys Arg Met Gln Lys Ala Asp Lys Thr Asp
145                 150                 155                 160
Ala Val Ile Lys Val Leu Asp Val Leu Phe Lys Ile Ile Asn Met Arg
                165                 170                 175
Ser
```

<210> 12
<211> 227
<212> PRT
<213> Streptococcus pyogenes

<400> 12

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Met Ala Lys Asn Asn Thr Asn Arg His Tyr Ser Leu Arg Lys Leu Lys
 1               5                  10                  15
Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu Lys Ala Arg
            20                  25                  30
Thr Gly Thr Ala Ser Val Ala Val Ala Leu Thr Val Leu Gly Ala Gly
        35                  40                  45
Phe Ala Asn Gln Thr Glu Leu Glu Asn Ala Met Glu Val Ala Gly Arg
    50                  55                  60
Asp Phe Lys Arg Ala Glu Glu Leu Glu Lys Ala Lys Val Lys Ala Asn
65                  70                  75                  80
Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn Asn
                85                  90                  95
Pro Ala Gln Ala Leu Glu Asp Gln Arg Lys Asp Leu Glu Thr Lys Leu
            100                 105                 110
Lys Glu Leu Gln Gln Asp Tyr Asp Leu Ala Lys Glu Ser Thr Ser Trp
        115                 120                 125
Asp Arg Gln Arg Glu Glu Lys Lys Lys Ala Leu Glu Leu Ala Ile Asp
    130                 135                 140
Gln Ala Ser Gln Leu Glu Lys Glu Leu Glu Glu Lys Lys Glu Ala Asp
145                 150                 155                 160
Tyr Asn Arg Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg
                165                 170                 175
Glu Gln Glu Ile Asn Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg Asp
            180                 185                 190
Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Arg Asn Leu Leu Gly
        195                 200                 205
Asn Ala Lys Leu Glu Leu Asp Gln Leu Ser Ser Glu Lys Glu Gln Leu
    210                 215                 220
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Thr Ile Arg
225

<210> 13
<211> 199
<212> PRT
<213> Unknown

<220>
<223> Sequence 1 from WO 97/01638

<221> VARIANT
<222> (1)...(199)
<223> Xaa = Any Amino Acid

<400> 13

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Met Lys Asn Ile Gly Tyr Ile Phe His His Pro Asp Arg Gln Ala Val
 1               5                  10                  15
Ala Ala Lys Val Thr Ala Leu Ala Leu Gly Ile Ala Leu Ala Ser Gly
            20                  25                  30
Tyr Ala Ser Ala Glu Glu Lys Asp Lys Leu Asp Ala Glu Phe Lys Pro
        35                  40                  45
Val Ala Glu Lys Leu Ala Ala Ser Lys Ile Ala Phe Ile Asn Ala Lys
    50                  55                  60
Glu Val Asp Asp Lys Ile Ala Ala Ala Arg Lys Lys Val Glu Ala Lys
65                  70                  75                  80
Val Ala Ala Leu Glu Lys Asp Ala Pro Arg Leu Arg Gln Ala Asp Ile
                85                  90                  95
Gln Lys Leu Leu Asp Ser Ile Gln Thr Ala Thr Asn Asn Leu Ala Arg
            100                 105                 110
Arg Gln Glu Glu Ile Asn Lys Leu Gly Ala Ala Glu Asp Ala Glu Leu
        115                 120                 125
Gln Lys Leu Met Gln Glu Ala Lys Gly Tyr Thr Tyr Val Leu Asp Ala
    130                 135                 140
Asn Ser Val Val Phe Ala Val Glu Gly Gln Asp Lys Lys Val Gln Glu
145                 150                 155                 160
Phe Gln Ala Gln Asn Glu Lys Arg Gln Ala Glu Glu Arg Gly Lys Lys
                165                 170                 175
Asp Ile Thr Glu Glu Val Leu Lys Ser Ile Pro Ala Ser Glu Lys Ala
            180                 185                 190
Gln Phe Lys Lys Xaa Xaa Val
        195
```